cells with PE-labeled goat anti-human Ig to detect chimeric SDF-Fc polypeptide remaining after the 3- or 15-hour incubation (data not shown).

Down-regulation of receptor by binding of MIP-1 α -Fc and MIP-1 β -Fc chimeric polypeptides to cells is determined by an assay for receptor down-regulation analogous to that described above.

SEQUENCE LISTING

10	(1) GENE	RAL INFORMATION:
	(i)	APPLICANT: Herrmann, Steve Swanberg, Stephen
15	(ii)	TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING CHEMOKINE DOMAINS
	(iii)	NUMBER OF SEQUENCES: 10
20	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Genetics Insititute, Inc. (B) STREET: 87 CambridgePark (C) CITY: Cambridge
25		(C) CITT: Cambridge (D) STATE: MA (E) COUNTRY: USA (F) ZIP: 02140
30	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
35	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
40	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Sprunger, Suzanne (B) REGISTRATION NUMBER: P-41,323 (C) REFERENCE/DOCKET NUMBER: GI5291
45	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (617) 498-8284 (B) TELEFAX: (617) 876-5851
50	(2) INFO	RMATION FOR SEQ ID NO:1:
<i>_</i>	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 328 amino acids

5

(B) TYPE: amino acid(C) STRANDEDNESS:(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

										٠						
10	(xi)	SEQU	JENCE	E DES	CRIE	OITS	1: SE	EQ II	ONO	:1:						
	Met 1	Asn	Ala	Lys	Val 5	Val	Val	Val	Leu	Val 10	Leu	Val	Leu	Thr	Ala 15	Leu
15	Cys	Leu	Ser	Asp 20	Gly 、	Lys	Pro	Val	Ser 25	Leu	Ser	Tyr	Arg	Cys 30	Pro	Cys
	Arg	Phe	Phe 35	Glu	Ser	His	Val	Ala 40	Arg	Ala	Asn	Val	Lys 45	His	Leu	Lys
20	Ile	Leu 50	Asn	Thr	Pro	Asn	Cys 55	Ala	Leu	Gln	Ile	Val 60	Ala	Arg	Leu	Lys
25	Asn 65	Asn	Asn	Arg	Gln	Val 70	Cys	Ile	Asp	Pro	Lys 75	Leu	Lys	Trp	Ile	Gln 80
	Glu	Tyr	Leu	.Glu	Lys 85	Ala	Leu	Asn	Lys	Gly 90	Ser	Gly	Ser	Gly	Ser 95	Gly
30	Ser	Gly	Ser	Glu 100	Ser	Lys	Tyr	Gly	Pro 105	Pro	Cys	Pro	Ser	Cys 110	Pro	Ala
3 E	Pro	Glu	Phe 115	Glu	Gly	Ala	Pro	Ser 120	Val	Phe	Leu	Phe	Pro 125	Pro	Lys	Pro
35	Lys	Asp 130	Thr	Leu	Met	Ile	Ser 135	Arg	Thr	Pro	Glu	Val 140	Thr	Cys	Val	Val
40	Val 145	Asp	Val	Ser	Gln	Glu 150	Asp	Pro	Glu	Val	Gln 155	Phe	Asn	Trp	Tyr	Val 160
	Asp	Gly	Val	Glu	Val 165	His	Asn	Ala	Lys	Thr 170	Lys	Pro	Arg	Glu	Glu 175	Gln
45	Phe	Asn	Ser	Thr 180	Tyr	Arg	Val	Val	Ser 185	Val	Leu	Thr	Val	Leu 190	His	Gln
5.0	Asp	Trp	Leu 195	Asn	Gly	Lys	Glu	Tyr 200	Lys	Cys	Lys	Val	Ser 205	Asn	Lys	Gly
50	Leu	Pro 210	Ser	Ser	Ile	Glu	Lys 215	Thr	Ile	Ser	Lys	Ala 220	Lys	Gly	Gln	Pro
55	Arg 225	Glu	Pro	Gln	Val	Tyr 230	Thr	Leu	Pro	Pro	Ser 235	Gln	Glu	Glu	Met	Thr 240
	Lys	Asn	Gln	Val	Ser 245	Leu	Thr	Cys	Leu	Val 250	Lys	Gly	Phe	Tyr	Pro 255	Ser
60	Asp	Ile	Ala	Val 260	Glu	Trp	Glu	Ser	Asn 265	Gly	Gln	Pro	Glu	Asn 270	Asn	Tyr
												_	_,		_	_

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

		275		280		285	
5		Arg Leu Th	_	ys Ser Arg	Trp Gln Glu 300	Gly Asn Val	Phe
5	Ser (Cys Ser Va		lu Ala Leu		Tyr Thr Gln	Lys 320
10	Ser I	Leu Ser Le	u Ser Leu G 325	ly Lys			
	(2) INFORM	MATION FOR	SEQ ID NO:	2:			
15	(i) S	(A) LENGT: (B) TYPE: (C) STRAM	HARACTERIST H: 1222 bas nucleic ac DEDNESS: do DGY: linear	e pairs id uble			
20	(ii) N	MOLECULE T	YPE: cDNA				
25	(rei) C	PEOTENCE DI	eccurpaton.	SEO ID NO.	o .		
				SEQ ID NO:		ACCGCGCTCT	60
		_				TTCTTCGAAA	120
30						AACTGTGCCC	180
						CCGAAGCTAA	240
35						GGGAGCGGCT	300
						CCAACCCAGG	360
						CAGGGACAGG	420
40						GTTCGAGGGG	480
						CTCCCGGACC	540
1 5						CCAGTTCAAC	600
· · ·						GGAGCAGTTC	660
						GCTGAACGGC	720
50						GAAAACCATC	780
				G CGAGGGCCAC			840
55							
5				r GCCAACCTCT			900
	•			C CCAGGAGGAG	•		960
50						GGGAGAGCAA	1020
	TGGGCAGCCG	GAGAACAAC	T ACAAGACCA	C GCCTCCCGTG	CTGGACTCCG	ACGGCTCCTT	1080

CTTCCTCTAC AGCAGGCTAA CCGTGGACAA GAGCAGGTGG CAGGAGGGGA ATGTCTTCTC 1140

	ATGO	CTCCGI	G AT	GCAT	GAGG	CTC	rGCAC	CAA C	CACT	ACAC	A CAG	GAAG	AGCC	TCT	CCT	STC	1200
	TCTC	GGTAA	A TG	ATAA	GAAT	TC											1222
5	(2)	INFO	RMATI	ON I	FOR S	SEQ 1	D NO):3:									
10		(i)	(B)	LEN TYI STI	E CHANGTH: PE: 8 RANDE	326 mino EDNES	ami aci	ino a id	S: ·· acids	3							·
		(ii)	MOLE	ECULI	TYI	E: p	prote	ein									
15																	
		(xi)	SEQU	JENCI	E DES	CRI	OITS	1: SI	EQ II	NO:	3:						
20		Met 1	Asn	Ala	Lys	Val 5	Val	Val	Val	Leu	Val 10	Leu	Val	Leu	Thr	Ala 15	Leu
		Cys _.	Leu	Ser	Lys 20	Pro	Val	Ser	Leu	Ser 25	Tyr	Arg	Cys	Pro	Cys 30	Arg	Phe
25		Phe	Glu	Ser 35		Val	Ala	Arg	Ala 40	Asn	Val	Lys	His	Leu 45	Lys	Ile	Leu
30		Asn	Thr 50	Pro	Asn	Cys	Ala	Leu 55	Gln	Ile	Val	Ala	Arg 60	Leu	Lys	Asn	Asn
		Asn 65	Arg	Gln	Val	Cys	Ile 70	Asp	Pro	Lys	Leu	Lys 75	Trp	Ile	Gln	Glu	Tyr 80
35		Leu	Glu	Lys	Ala	Leu 85	Asn	Lys	Gly	Ser	Gly 90	Ser	Gly	Ser	Gly	Ser 95	Gly
		Ser	Glu	Ser	Lys 100	Tyr	Gly	Pro	Pro	Cys 105	Pro	Ser	Cys	Pro	Ala 110	Pro	Glu
40		Phe	Glu	Gly 115	Ala	Pro	Ser	Val	Phe 120	Leu	Phe	Pro	Pro	Lys 125	Pro	Lys	Asp ,
45		Thr	Leu 130	Met	Ile	Ser	Arg	Thr 135	Pro	Glu	Val	Thr	Cys 140	Val	Val	Val	Asp
		Val 145	Ser	Gln	Glu	Asp	Pro 150	Glu	Val	Gln	Phe	Asn 155	Trp	Tyr	Val	Asp	Gly 160
50		Val	Glu	Val	His	Asn 165	Ala	Lys	Thr	Lys	Pro 170	Arg	Glu	Glu	Gln	Phe 175	Asn
		Ser	Thr	Tyr	Arg 180	Val	Val	Ser	Val	Leu 185	Thr	Val	Leu	His	Gln 190	Asp	Trp
55		Leu	Asn	Gly 195	Lys	Glu	Tyr	Lys	Cys 200	Lys	Val	Ser	Asn	Lys 205	Gly	Leu	Pro
60		Ser	Ser 210	Ile	Glu	Lys	Thr	Ile 215	Ser	Lys	Ala	Lys	Gly 220	Gln	Pro	Arg	Glu
		Pro 225	Gln	Val	Tyr	Thr	Leu 230	Pro	Pro	Ser	Gln	Glu 235	Glu	Met	Thr	Lys	Asn 240

	Gln	Val	Ser	Leu	Thr 245	Cys	Leu	Val	Lys	Gly 250	Phe	Tyr	Pro	Ser	Asp 255	Ile	
5	Ala	Val	Glu	Trp 260	Glu	Ser	Asn	Gly	Gln 265	Pro	Glu	Asn	Asn	Tyr 270	Lys	Thr	
	Thr	Pro	Pro 275	Val	Leu	Asp	Ser	Asp 280	Gly	Ser	Phe	Phe	Leu 285	Tyr	Ser	Arg	
10	Leu	Thr 290	Val	Asp	Lys	Ser	Arg 295	Trp	Gln	Glu	Gly	Asn 300	Val	Phe	Ser	Cys	
1 E	Ser 305	Val	Met	His	Glu	Ala 310	Leu	His	Asn	His	Tyr 315	Thr	Gln	Lys	Ser	Leu 320	
15	Ser	Leu	Ser	Leu	Gly 325	Lys											
	(2) INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:4:										
20	(i)	(A) LEI	E CHANGTH	: 12	16 ba	ase p		5								
25		(C)) STI) TOI	RANDI POLOC	EDNES	SS: 0 linea	doub.	le									
	(ii)	MOL	ECUĻI	E TYI	?E: (CDNA											
30								, 30. TI		4.							
				E DES							noom/	nama	7.000	7000	r Cm		60
35	GCGGCCGCC																
	GCCTCAGC																120
	TTGCCAGAC																180
40	TTGTAGCC																240
	TTCAGGAGT															;	300
45	CTGAGTCC	ra aa	ATGG	TCCC	CCA	rgcco	CAT	ATGT	CCAG	G TA	AGCC2	AACC	CAG	GCCT	CGC	-	360
40	CCTCCAGCT	C AA	\GGCG	GGAC	AGG:	rgcco	CTA C	AGTA	GCCT(G CA'	rcca(GGGA	CAG	GCCC	CAG	4	120
	CCGGGTGCT	rg ac	GCAT	CCAC	CTC	CATC	CT T	CCTC	'AGCA	C CT	GAGT'	rcga	GGG	GCA(CCA	4	180
50	TCAGTCTTC	CC TO	TTCC	CCCC	AAA	ACCC	AAG C	ACAC	TCTC	A TG	ATCT	CCCG	GAC	CCTC	GAG	!	540
	GTCACGTG	CG TO	GTGG	TGGA	CGT	GAGC	CAG C	GAAGA	CCCC	G AG	GTCC	AGTT	CAA	CTGGT	rac	(500
	GTGGATGG	CG TO	GAGG	TGCA	TAA!	rgcc?	AAG A	CAAA	GCCG	C GG	GAGG	AGCA	GTT	CAAC	AGC	(560
55	ACGTACCGT	rg Te	GTCA	.GCGT	CCT	CACC	STC (CTGCA	CCAG	G AC	TGGC'	TGAA	CGG	CAAGO	GAG	•	720
	TACAAGTG	CA AG	GTCT	CCAA	CAA	AGGC	CTC C	CCGTC	CTCC.	A TC	GAGA	AAAC	CAT	CTCC	AAA		780
60	GCCAAAGGT	rg go	ACCC	ACGG	GGT	GCGA	GGG (CACA	CGGA	C AG	AGGT	CAGC	TCG	GCCCI	ACC	8	340
	CTCTGCCC	rg go	AGTG	ACCG	CTG'	TGCC!	AAC (CTCTG	TCCC	T AC	AGGG	CAGC	CCC	GAGAC	GCC	9	900

	ACAGGTGTAC ACCCTGCCCC CATCCCAGGA GGAGATGACC AAGAACCAGG TCAGCCTGAC 960
	CTGCCTGGTC AAAGGCTTCT ACCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA 1020
5	GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT 1080
	CTACAGCAGG CTAACCGTGG ACAAGAGCAG GTGGCAGGAG GGGAATGTCT TCTCATGCTC 1140
10	CGTGATGCAT GAGGCTCTGC ACAACCACTA CACACAGAAG AGCCTCTCCC TGTCTCTGGG 1200
10	TAAATGATAA GAATTC · 1216
	(2) INFORMATION FOR SEQ ID NO:5:
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 331 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear
20	(ii) MOLECULE TYPE: protein
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
	Met Gln Vaí Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala 1 5 10 15
30	Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala 20 25 30
35	Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala 35 40 45
	Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe 50 55 60
40	Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp 65 70 75 80
45	Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Gly Ser Gly Ser' 85 90 95
	Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser 100 105 110
50	Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro 115 120 125
	Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr 130 135 140
55	Cys Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn 145 150 155 160
60	Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg 165 170 175
	Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val 180 185 190

	Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser 195 200 205
5	Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys 210 215 220
	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu 225 230 235 240
10	Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe 255
16	Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu 260 265 270
15	Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe 275 280 285
20	Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly 290 295 300
	Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr 305 310 315 320
25	Thr Gln Lys Ser Leu Ser Leu Gly Lys 325 330
	(2) INFORMATION FOR SEQ ID NO:6:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1234 base pairs (B) TYPE: nucleic acid
35	(C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
	GCGGCCGCCC AATCATGCAG GTCTCCACTG CTGCCCTTGC TGTCCTCCTC TGCACCATGG ' 60
45	CTCTCTGCAA CCAGTTCTCT GCATCACTTG CTGCTGACAC GCCGACCGCC TGCTGCTTCA 120
	GCTACACCTC CCGGCAGATT CCACAGAATT TCATAGCTGA CTACTTTGAG ACGAGCAGCC 180
50	AGTGCTCCAA GCCCGGTGTC ATCTTCCTAA CCAAGCGAAG CCGGCAGGTC TGTGCTGACC 240
J 0	CCAGTGAGGA GTGGGTCCAG AAATACGTCA GTGACCTGGA GCTGAGTGCC GGATCCGGCT 300
	CTGGGAGCGG CTCTGGCTCT GAGTCCAAAT ATGGTCCCCC ATGCCCATCA TGTCCAGGTA 360
55	AGCCAACCCA GGCCTCGCCC TCCAGCTCAA GGCGGGACAG GTGCCCTAGA GTAGCCTGCA 420
	TCCAGGGACA GGCCCCAGCC GGGTGCTGAC GCATCCACCT CCATCTCTTC CTCAGCACCT 480
60	GAGTTCGAGG GGGCACCATC AGTCTTCCTG TTCCCCCCAA AACCCAAGGA CACTCTCATG 540
	ATCTCCCGGA CCCCTGAGGT CACGTGCGTG GTGGTGGACG TGAGCCAGGA AGACCCCGAG 600
	GTCCAGTTCA ACTGGTACGT GGATGGCGTG GAGGTGCATA ATGCCAAGAC AAAGCCGCGG 660

	GAGGAGCAGT TCAACAGCAC GTACCGTGTG GTCAGCGTCC TCACCGTCCT GCACCAGGAC 720
	TGGCTGAACG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA AAGGCCTCCC GTCCTCCATC 780
5	GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCACGGGG TGCGAGGGCC ACACGGACAG 840
	AGGTCAGCTC GGCCCACCCT CTGCCCTGGG AGTGACCGCT GTGCCAACCT CTGTCCCTAC 900
10	AGGGCAGCCC CGAGAGCCAC AGGTGTACAC CCTGCCCCCA TCCCAGGAGG AGATGACCAA 960
10	GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA 1020
	GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC 1080
15	CGACGGCTCC TTCTTCCTCT ACAGCAGGCT AACCGTGGAC AAGAGCAGGT GGCAGGAGGG 1140
	GAATGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA CACAGAAGAG 1200
20	CCTCTCCCTG TCTCTGGGTA AATGATAAGA ATTC 1234
	(2) INFORMATION FOR SEQ ID NO:7:
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 331 amino acids (B) TYPE: amino acid (C) STRANDEDNESS:
30	(ii) MOLECULE TYPE: protein
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
	1 5 10 15
40	Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr 20 25 30
	Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
45	Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val 50 55 60
5 0	Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser 65 70 75 80
50	Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn Gly Ser Gly Ser 85 90 95
55	Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
	Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro 115 120 125
60	Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr 130 135 140
	Cys Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn

	145					150					155					160
5	Trp	Tyr	Val	Asp	Gly 165	Val	Glu	Val	His	Asn 170	Ala	Lys	Thr	Lys	Pro 175	Arg
5	Glu	Glu	Gln	Phe 180	Asn	Ser	Thr	_	Arg 185	Val	Val	Ser	Val	Leu 190	Thr	Val
10	Leu	His	Gln 195	Asp	Trp	Leu	Asn	Gly 200	Lys	Glu	Tyr	Lys	Cys 205	Lys	Val	Ser
	Asn	Lys 210	Gly	Leu	Pro	Ser	Ser 215	Ile	Glu	Lys	Thr	Ile 220	Ser	Lys	Ala	Lys
15	Gly 225	Gln	Pro	Arg	Glu `	Pro 230	Gln	Val	Tyr	Thr	Leu 235	Pro	Pro	Ser	Gln	Glu 240
20	Glu	Met	Thr	Lys	Asn 245	Gln	Val	Ser	Leu	Thr 250	Cys	Leu	Val	Lys	Gly 255	Phe
20	Tyr	Pro	Ser	Asp 260	Ile	Ala	Val	Glu	Trp 265	Glu	Ser	Asn	Gly	Gln 270	Pro	Glu
25	Asn	Asn	Tyr 275	Lys	Thr	Thr	Pro	Pro 280	Val	Leu	Asp	Ser	Asp 285	Gly	Ser	Phe
	Phe	Leu 290	Tyŗ	Ser	Arg	Leu	Thr 295	Val	Asp	Lys	Ser	Arg 300	Trp	Gln	Glu	Gly
30	Asn 305	Val	Phe	Ser	Cys	Ser 310	Val	Met	His	Glu	Ala 315	Leu	His	Asn	His	Tyr 320
35	Thr	Gln	Lys	Ser	Leu 325	Ser	Leu	Ser	Leu	Gly 330	Lys					
J J	(2) INFO	RMAT	ON F	FOR S	SEQ I	D NC	8:									
40	(i)	(B)	LEN	IGTH: PE: II LANDE	123 ucle	s ba sic a ss: d	se p cid loubl	airs								,
45	(ii)	MOLE	CULE	TYP	E: c	:DNA										
	(xi)	SEQU	JENCE	DES	CRIP	TION	: SE	Q ID	NO:	8:						
50	GCGGCCGCC	A AT	ACCAT	rgaa.	GCTC	TGCG	TG A	CTGT	CTGI	r CTC	TCCT	CAT	GCTA	GTAG	CT	60
	GCCTTCTGC	T CT	CCAG	CGCT	CTCA	GCAC	CA A'	rggg(CTCAG	ACC	CTCC	CAC	CGCC	TGCT	GC	120
55	TTTTCTTAC	A CC	GCGAC	GAA	GCTT	CCTC	GC A	ACTT1	GTGG	TAG	ATTA	CTA	TGAG	ACCA	.GC	180
	AGCCTCTGC	T CC	CAGC	CAGC	TGTG	GTAT	TC C	AAACO	AAAA	A GAA	.GCAA	GCA	AGTC	TGTG	CT	240
60	GATCCCAGI	'G AA'	rccto	GGT	CCAG	GAGT	AC G	IGTAI	GACC	TGG	AACT	GAA	CGGA	TCCG	GC	300
	TCTGGGAGC	G GC	rctgo	CTC	TGAG	TCCA	AA T	ATGGT	CCCC	CAT	GCCC	ATC	ATGT	CCAG	GT	360
	AAGCCAACC	C AG	GCCTC	CGCC	CTCC	AGCT	CA A	GCGG	GACA	GGT	GCCC	TAG	AGTA	GCCT	GC	420

	ATCCAGGGAC AGGCCCCAGC CGGGTGCTGA CGCATCCACC TCCATCTCTT CCTCAGCACC 480	***
	TGAGTTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCCA AAACCCAAGG ACACTCTCAT 540	
5	GATCTCCCGG ACCCCTGAGG TCACGTGCGT GGTGGTGGAC GTGAGCCAGG AAGACCCCGA 600	
	GGTCCAGTTC AACTGGTACG TGGATGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG 660	
10	GGAGGAGCAG TTCAACAGCA CGTACCGTGT GGTCAGCGTC CTCACCGTCC TGCACCAGGA 720	
10	CTGGCTGAAC GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC AAAGGCCTCC CGTCCTCCAT 780	
	CGAGAAAACC ATCTCCAAAG CCAAAGGTGG GACCCACGGG GTGCGAGGGC CACACGGACA 840	
15	GAGGTCAGCT CGGCCCACCC TCTGCCCTGG GAGTGACCGC TGTGCCAACC TCTGTCCCTA 900	
	CAGGGCAGCC CCGAGAGCCA CAGGTGTACA CCCTGCCCCC ATCCCAGGAG GAGATGACCA 960	
20	AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC ATCGCCGTGG 1020	
	AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC GTGCTGGACT 1080	
٠	CCGACGGCTC CTTCTTCCTC TACAGCAGGC TAACCGTGGA CAAGAGCAGG TGGCAGGAGG 1140	
25	GGAATGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC ACACAGAAGA 1200	
	GCCTCTCCCT GTCTCTGGGT AAATGATAAG AATTC 1235	
30	(2) INFORMATION FOR SEQ ID NO:9:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 amino acids	
	(B) TYPE: amino acid (C) STRANDEDNESS:	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
4.5	Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala	
45	1 5 10 15	
	Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala 20 25 30	
50	Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala	
	35 40 45	
55	Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe 50 55 60	
33	Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp	
	65 70 75 80	
60	Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala 85 90	
	(2) INFORMATION FOR SEQ ID NO:10:	

5	(i)	(A (B (C		NGTH PE: RAND	: 92 amin EDNE	ami o ac SS:	no a id									
	(ii)	MOL	ECUL	E TY	PE:]	prot	ein	••			··		••••			•
10				-												
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	ON O	:10:						
15	Met 1	Lys	Leu	Cys	Val 5	Thr	Val	Leu	Ser	Leu 10	Leu	Met	Leu	Val	Ala 15	Ala
	Phe	Cys	Ser	Pro 20	Ala	Leu	Ser	Ala	Pro 25	Met	Gly	Ser	Asp	Pro	Pro	Thr
20	Ala	Cys	Cys 35	Phe	Ser	Tyr	Thr	Ala 40	Arg	Lys	Leu	Pro	Arg 45	Asn	Phe	Val
25	Val	Asp 50	Tyr	Tyr	Glu	Thr	Ser 55	Ser	Leu	Cys	Ser	Gln 60	Pro	Ala	Val	Val
23	Phe 65	Gln	Thr	Lys	Arg	Ser 70	Lys	Gln	Val	Cys	Ala 75	Asp	Pro	Ser	Glu	Ser 80
30	Trp	Val	Gln	Glu	Tyr 85	Val	Tyr	Asp	Leu	Glu 90	Leu	Asn				

--

 $oldsymbol{\cdot}$

.•